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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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50K glycoprotein p
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Ig kappa chain V-J
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A;Accession: A53287 A;Status: not compared with cc A;Wolecule type: mRNA A;Residues: 250-264,'W',266-28 A;Note: sequence extracted fro R;Edwards, M.C.; Gibbs, R.A. Genomics 14, 590-597, 1992 A;Title: A human dimorphism re A;Reference number: I54176; MU A;Accession: I54176 A;Status: translated from GB/E	A;Title: Protein and A;Reference number: A;Reference number: A;Contents: disulfic A;Accession: A34194 A;Accession: A3494 A;Molecule type: px A;Residues: 26-394 A;Lederman, S.; DeMa R;Lederman, S.; D	A;Title: Corrected CD4 seque: A;Reference number: A90907; I A;Contents: annotation; revi R;Camerini, D.; Seed, B. Cell 60, 747-754, 1990 A;Title: A CD4 domain import. A;Reference number: A32722; I A;Accession: A32722 A;Accession: A32722 A;Accession: A32722 A;Status: nucleic acid seque: A;Molecule type: mRNA A;Residues: 26-426,428-458  R;Carr, S.A.; Hemling, M.E.; J. Bill Chem 264 21266-213.	RESULT 1  RWHUT4  T-cell surface glycoprotein CD4 pr. T-cell surface: N;Alternate names: T-cell surface: C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence revi C;Accession: A90872; A32722; A3419. C;Accession: A90872; Littman, D.R.; God Cell 42, 93-104, 1995 A;Title: The isolation and nucleot. A;Title: The isolation and nucleot. A;Reference number: A90872; MUID:8 A;Accession: A90872 A;Molecule type: mRNA A;Residues: 1-25; NY,27-458 <mad> A;Cross-references: UNIPROT:P01730 A;Experimental source: clone pT4B R;Littman, D.R.; Maddon, P.J.; Axe. Cell 35, 541 1988</mad>	30 108.5 10 31 108 10 32 107.5 10 33 106.5 10 34 106.5 10 35 106.5 10 36 106.5 10 37 106.5 10 39 105 10 39 105 10 41 103.5 10 42 103.5 10 44 103.5 10 45 103.5 10
nceptual tr 10 <led> m NCBI back 15 USBI back 15 USBI back 16 USBI back 17 USBI back</led>	A;Title: Protein and Carbohydrate structura A;Reference number: A34194; MUID: 90078232; A;Contents: disulfide bonds; carbohydrate-b A;Accession: A34194 A;Molecule type: protein A;Residues: 26-394 <car> A;Residues: 26-394 <car> R;Lederman, S.; DeMartino, J.A.; Daugherty, Mol. Immunol. 28, 1171-1181, 1991 A;Title: A single amino acid substitution i A;Reference number: A53287; MUID: 92072595;</car></car>	nce. MUID:89028665; MUID:8028665; ant for HIV-med MUID:90182664; nce not shown; CAM> Folena-Wasserm	rotein CD4 precursor   cell surface antigen 7 cell surface antigen 7 sequence revision 31-1 sa2722; \$\bar{A}34194; A53287 an, D.R.; Godfrey, M.; and nucleotide seque 90872; MUID:85254948; 90872; MUID:85254948; 27-458 <mad> NIFROT:PO1730 clone pT4B on, P.J.; Axel, R.</mad>	5 333 2 A31923 5 257 2 S00682 4 122 2 S40370 3 111 2 I387266 3 111 2 I39740 3 584 2 I50419 3 773 1 QRRBG 3 345 2 JC4025 647 2 B41288 2 647 2 B41288 1 103 2 S18731 1 108 1 KVMS06 1 117 2 S21668 1 119 1 KIHUWK 0 1028 2 A53449
ation (NCBIP:	ral analysis of a recombinant soluble CD4 recept pMID:2592374 -binding sites  y, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary, A in a common African allele of the CD4 molecule; PMID:1961196	PMID:3263213 2 26 26 Riliated syncytium formation lies outside the vi: PMID:2107024 Rot compared with conceptual translation Rot compared with conceptual translation	or [validated] - human on T4/Leu 3 11-Dec-1988 #text change 09-Jul-2004 1287; I54176; I54797; A02109; A30039 M.; Maddon, D.B.; Chess, L.; Axel, R. squence of a cDNA encoding the T cell surface prot	amalgam protein pr IgE Fc receptor al Ig kappa chain - h Ig kappa chain V r Ig kappa chain V r Ig kappa chain V v s-gicerin precurso secretory componen opioid-binding pro opioid-binding cel vascular cell adhe biliary glycoprote Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain pre plasmacytoma-assoc

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C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A;Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the A;Reference number: A32722; MUID:90182664; PMID:2107024
A;Accession: B32722.
                                                                                                                                                                                                                        C;Species: Pan troglodytes (chimpanzee,
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B32722; A46534
            A;Cross-references: UNIPROT:P16004; GB:M31135
R;Fomsgaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules:
A;Reference number: A46534; MUID:93049640; PMID:1425921
A;Accession: A46534
 A;Status:
                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-432 < CAM>
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Hum. Immunol. 30, 99-104, 1991
A;Title: Humans with OKT4-epitope deficiency have a single nucleotide base change in A;Reference number: I54297; MUID:91216786; PMID:1708753
A;Accession: I54297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: GB:U47924; GB:M86525; GB:U72506; NID:g1633547; PIDN:AAB51309.1;
D:Hodge. T.W.; Sasso, D.R.; McDougal, J.S.
                                                                                                                                                                                                                                                                                                                 T-cell surface glycoprotein CD4 - chimpanzee
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Best Local Sim
Matches 199;
                                                                                                                                                                                                                                                                               ;Alternate names: T-cell surface antig;Species: Pan troglodytes (chimpanzee)
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compared with
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conceptual
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Pred. No. 2.1e-75;
0; Mismatches 1
translation
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A; Molecule type: mRNA
A, Residues: 3-399 <FOM>
A, Residues: 3-399 <FOM>
A; Note: sequence extracted from NCBI backbone (NCBIP:118332)
A; Note: sequence extracted from NCBI backbone (NCBIP:118332)
C; Comment: This protein is expressed on most thymocytes, on a subset of maticity of the protein of the protein CD4; immunoglobulin homology
C; Keywords: duplication; glycoprotein; T-cell; transmembrane protein
F; 1-437/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F; 1-371/Domain: extracellular #status predicted <EXT>
F; 9-86/Domain: immunoglobulin homology *IMI>
F; 191-274/Domain: immunoglobulin homology *IM3>
F; 291-274/Domain: immunoglobulin homology <IM3>
F; 296-347/Domain: immunoglobulin homology <IM3>
F; 372-395/Domain: transmembrane #status predicted <INT>
F; 16-84,130-159,303-345/Disulfide bonds: #status predicted
F; 271,300/Binding site: carbohydrate (Asm) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                    F;111-161/Domain: immunoglobulin homology #status atypical <IM2>F;180-293/Domain: immunoglobulin homology <IM3>F;296-347/Domain: immunoglobulin homology <IM3>F;296-347/Domain: immunoglobulin homology <IM4>F;372-395/Domain: transmembrane #status predicted <IMM>F;372-395/Domain: intracellular #status predicted <INT>F;36-432/Domain: intracellular #status predicted <INT>F;16-84,130-159,300-345/Disulfide bonds: #status predicted F;16-84,130-159,300-345/Disulfide bonds: #status predicted F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Comment: This protein is expressed on most thymocytes, on a subset of C;Comment!y: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT's F;1-371/Domain: extracellular #status predicted <EXT's F;1-86/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 60, 747-754, 1990
A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024
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A; Residues: 1-432 < CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C32722
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Best Local S
Matches 170
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                                                                                                               KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL
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                                                                                   KVVLGKKGDTVELTCTASOKKNTOFHWKNSNOIKILGIQGLFLTKGPSKLSDRADSRKSL
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97.7%;
                                                                                                                                                                                                                       76.8%; Score 790; DB 1; 87.4%; Pred. No. 1.5e-56;
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Pred. No. 1.9e-63;
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CD4 precursor - 1
C;Species: Orycto
C;Date: 21-Sep-19
C;Accession: A463
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A;Title: CD4 and its role in infection of rabbit cell lines by human immunodeficiency vi A;Reference number: A46254; MUID:92390370; PMID:1518821
A;Reteus: preliminary
A;Rolecule type: mRNA
A;Residues: preliminary
A;Rolecule type: mRNA
A;Residues: 1-459 <HAG-
A;Cross-references: UNIPROT:P46630; GB:M92840; NID:g164871; PIDN:AAA31198.1; PID:g164872
A;Note: sequence extracted from NCBI backbone (NCBIN:112732, NCBIP:112733)
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
F;322-372/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                        A;Cross-references: EMBL:X68565; NID:g288652; PIDN:CAB37664.1; C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                         T-cell surface glycoprotein CD4 - dog
(;Species: Canis lupus familiaris (dog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: $30193
R;Milde, K.F.; Conner, G.B.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A;Title: Primary structure of the canine CD4 antigen.
A;Reference number: $30193; MUID:93192324; PMID:7916632
A;Accession: $30193.
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A;Molecule type: mRNA
A;Residues: 1-432 <MIL>
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Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
                                                                                Matches
                                                                                                                                                            202-311/Domain:
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Best Local Similarity
Matches 120; Conserva
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                        LVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTK
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LMLQLVMLPAVTPVREVVLGKAGDAVELFCQTSQKKNIHFNWRDSSMVQILGNQGSFWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDSGTWSCHLSFQDQNKLELDIKII 205
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                                                                                                                                                            immunoglobulin homology <IMM>
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                                                                                                54.6%;
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                                                                            Score 562; DB 2;
Pred. No. 4.6e-38;
7; Mismatches 42
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Pred. No. 4.2e-40;
                                                                                42;
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                                                                                                                 Length 432;
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homology
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T-cell surface glycoprotein CD4 precursor - mouse
N;Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen
C;Species: Mus musculus (house revision 30-Jun-1987 #text change 09-Jul-2004
C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R.
A; Accession: A02110
A; Molecule type: mRI
A; Residues: 1-457 <
                                                                             R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. Science 234, 610-614, 1986
A;Title: Isolation and sequence of L3T4 complementary DNA clones: expression A;Reference number: A02110; MUID:87018845; PMID:3094146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P05540; GB:M15768; NID:g203387; PIDN:AAA40901.1; PID:g203388 R;Davis, S.J.; Ward, H.A.; Puklavec, M.J.; Willis, A.C.; Williams, A.F.; Barclay, A.N. J. Biol. Chem. 265, 10410-10418, 1990 A;Title: High level expression in Chinese hamster ovary cells of soluble forms of CD4 T A;Reference number: A35433; MUID:90285164; PMID:2113054 A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F. Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987
A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: evidence A;Reference number: A27449; MUID:87175535; PMID:3104900
A;Accession: A27449
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A27449
T-cell surface glycoprotein CD4 precursor -
T,cell surface glycoprotein CD4 precursor -
N;Alternate names: W3/25 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1988 #sequence revision 21-Ma
C;Accession: A27449; A35433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-457 < CLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNRGVPFRHL--LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DSGIWNCTVTLNQKKHSFDMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSGTWTCTVLQNQKKVEFKIDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTVLQNQKKVEFKIDIV 200
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49.0%; Pre
ative 34;
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Pred. No. 4.5e-32;
4; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
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1987
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A;Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1; PID:g554183
R;Classon, B.J.; Tsagaratos, J.; Kirszbaum, L.; Maddox, J.; Mackay, C.R.; Bra Immunogenetics 23, 129-132, 1986
A;Title: The L3T4 antigen in mouse and the sheep equivalent are immunoglobuli A;Reference number: A47642; MUID:8616694; PMID:3082751
A;Reference number: A47642; MUID:8616694; PMID:3082751
A;Rocession: A47642
A;Molecule type: protein
A;Residues: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of maturatives: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of maturatives: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of maturatives: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of maturatives: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of maturative introducting supportein CD4; immunoglobulin homology
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; transnatives: 27-45/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;25-114/Domain: immunoglobulin homology <IM13>
F;21-37/Product: CD4, brain-specific short form #status predicted <BRA>
F;321-372/Domain: immunoglobulin homology <IM4>
F;321-372/Domain: immunoglobulin homology <IM4+
F;321-372/
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F;420-457/Domain: intracellular #status predicted <INT>
F;42-112,159-188,328-370/Disulfide bonds: #status predicted
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A;Molecule type: DNA
A;Residues: 1-25,'E',27-457 <GOR>
A;Residues: 1-25,'E',27-457 <GOR>
A;Cross-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID:g387124
R;Maddon, P.J.; Molineaux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey, M.; Alt, F.W.;
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
A;Title: Structure and expression of the human and mouse T4 genes.
A;Reference number: A39955; MUID:88097446; PMID:3501122
A;Accession: A39955
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R;Gorman, S.D.; Tourviellle, B.; Parnet, Pioc. Natl. Acad. Sci. U.S.A. 84, 7644-7.548, 1987
A;Title: Structure of the mouse gene encoding CD4 and an unusual transcript A;Reference number: A39893; MUID:88041159; PMID:2823269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 208-318 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: I69018
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-457 < RES>
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Immunol. Rev. 100, 109-127, 19871
A;Title: L3T4 and the immunoglobulin gene superfamily: 1
A;Reference number: I54564; MUID:88152875; PMID:3326818
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Littman, D.R.; Gettner, Nature 325, 453-455, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M36850; NID:g198670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: the cited GenBank accession number, J03564, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 25-457 < MAD>
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A; Residues: 1-457 <LIT>
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                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                            187,298,323,392/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment: This protein is expressed on most thymocytes, on a subset of mature
                                                                                                                                                                                                                                                                     Local Similarity
       6
KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                              MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI
                                                                       MCRAISLRRLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     46.2%;
                                                                                                                                                                                                                                                                 Score 475; DB 1;
Pred. No. 5.5e-31;
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                                                                                                                                                                                                                                                                                                     Length 457;
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RESULT 9
821461
7-cell surface glycoprotein CD4 (allele 1) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change
C;Accession: 147131; S21461
C;Accession: K: Germana, S.; Sundt, T.M.
                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q29027; EMBL:X65629; NID:g1928; PIDN:CAA46583.1; C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: glycoprotein; T-cell
                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Extensive allelic polymorphism in A;Reference number: I47131; MUID:93329116; A;Accession: I47131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Gustafsson, K.; Germana, S.; Sundt, T.M. J. Immunol. 151, 1365-1370, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: Iódorov, A.V.; Nedospasov, S.A.; Maliushova, V.V.; Udalova, I.A.;
Vopr. Virusol. 40, 100-102, 1995
A;Title: [Nuclociide sequence of two exons of the human T-lymphocyte CD4 receptor A;Reference number: Iódo82; MUID:95407135; PMID:7676667
A;Accession: Iódo82
                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-99 < GU2>
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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues:
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A;Residues: 1-71 <RES>
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Best Local
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Species: Homo sapiens (man)
                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ILGNQGSFLTK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                        59;
                                                                                                                                 Similarity
KAGDLAELPCHSSOKKNLPFNWKNSNOTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG
                                              KKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFL-TKGPSKLNDRADSRRSLWDOG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILGQHGKGVLIRGGSPSQF-DRFDSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKE
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                                                                                                                                                                                                         immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                   translated from GB/EMBL/DDBJ
                                                                                                   29.7%; Score 305.5; DB 2; 60.2%; Pred. No. 5e-18; tive 16; Mismatches 22;
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Pred. No. 2.3e-22;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                        the CDR2-like PMID:8335933
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60
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В

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vascular cell adhesion protein - pig
(;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_chan
C;Accession: JC2457
R;Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
Blochem. Blophys. Res. Commun. 201, 805-812, 1994
A;Ttlle: Cloning and expression kinetics of porcine vascular
A;Reference number: JC2457; MUID:94271236; PMID:7516159
A;Accession: JC2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gustafsson, K.; Germana, S.; Sundt, T.M.
J. Immunol. 151, 1365-1370, 1993
A;Title: Extensive allelic polymorphism in the CDR2-like
A;Reference number: 147131; MUID:93329116; PMID:8335933
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A; Residues: 1-538 < TSA>
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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: glycoprotein; T-cell
E;3-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 <GU2>
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                  Keywords: glycoprotein; transmembrane protein; Keywords: glycoprotein; transmembrane #status predicted <TWM>;75,157,271,330,360/Binding site: carbohydrate (Asn) (
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                                                                                                                                                ATLTLIAMRMEDSGIYVCEGVNPVGTNRKEVELTVQVAPRDTTISVNPSSTLEEGSSVNM
                                                                                                                                                                                   FPLIIKNLKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQSLTL
                                                                                                                                                                                                                        QEGDSMMTCTSEGLPAPQISW----SGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP-SKLNDRADSRRSLWDQG
                                     BFKI 197
                                                                                                         TLESPPGSSPSV----QCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ----NQKKV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAGDLAELPCHSSQKKNLPFSWKNSDQIKILRSHRNLWHKASVTELSSRLDSKKNMWDHG
 ELII
                                                                        TCSSDGFPAPKILWSKKLRDGNLEPLSENTTLTLTSTKMEDSGIYVCEGINQAGINRKEV
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395
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                                                                                                                                                                                                                                                                                                  37;
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Pred. No. 5.3e-16;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                Score 140.5; DB 2;
Pred. No. 0.00089;
7; Mismatches 62;
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A;Molecule type: mRNA,
A;Residues: 1159-1199,'G',1201-1235,'K',1237 <PRI>
A;Note: this paper appeared earlier, with printing errors, as reference A30326
A;Prince, J.T.; Milona, N.; Stallcup, W.B.
J. Neurosci. 9, 876-883, 1989
A;Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identific A;Reference number: A30336; MUID:89177485; PMII:2466566
A;Contents: annotation
A;Note: this paper was reprinted as reference A60917 to correct the omission of several if C;Comment: This sequence of this surface-accessible glycoprotein differs at only two possaccessible only after treatment of cells with detergent and is assumed to be cytoplasmic C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; in C;Keywords: cell adhesion; duplication; glycoprotein; membrane protein
C;Keywords: cell adhesion; duplication; glycoprotein; membrane protein
vascular cell adhesion molecule-1 precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004 C;Accession: JS0675; S19872; S23136 R;Hession, C.; Moy, P.; Tizard, R.; Chisholm, P.; Williams, C.; Wysk, M.; Burkly, Biochem. Biophys. Res. Commun. 183, 163-169, 1992 Biochem. Biophys. Res. Commun. 183, 163-169, 1992 A;Title: Cloning of murine and rat vascular cell adhesion molecule-1.
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A;Accession: S17655
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1178,1183-1259 <MI2>
A;Cross-references: EMBL:X59149; NID:g56740; PIDN:CAA41860.1;
A;Cross-references: EMBL:X59149; PIDN:CAA41860.1;
A;Cross-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neural cell adhesion molecule L1 - rat
N;Alternate names: nerve growth factor-inducible large external glycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S36126; S17655; A60917; A30326
R;Miura, M.; Kobayashi, M.; Asou, H.; Uyemura, K.
FEBS Lett. 289, 91-95, 1991
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A; Residues: 1-12
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                                                                                                                                                                                                                                                                                                                                                                                                        JS0675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGKV----PGNOTSTTLKLSPYVHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2, 'G', 4-121, 'HL',124-165, 'N',167-738, 'G' <WIL>
A;Residues: 1-2, 'G', 4-121, 'HL',124-165, 'N',167-738, 'G' <WIL>
A;Residues: 1-2, 'G', 4-121, 'RID:957471; PIDN:CAA45544.1; PID:957472
A;Cross-references: EMBL:X63722; NID:957471; PIDN:CAA45544.1; PID:957472
A;Cross-references: EMBL:X63722; NID:957471; PIDN:CAA45544.1; PID:957472
A;Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.
Biophys. Acta 1131, 214-216, 1992
A;Title: Nuclectide sequence of rat vascular cell adhesion molecule-1 cDNA.
A;Reference number: S23136; MUID:92305064; PMID:1377031
A;Recession: S23136
A;Recession: S23136
A;Recession: S23136
A;Recession: S23136
A;Residues: 1-2, 'G', 4-165, 'N', 167-738, 'G' <WI2>
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2, 'G', 4-165, 'N', 167-738, 'G' <WI2>
C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late antigen 4 or C;Comment: This protein integrin very late
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A;Cross-references: UNIPROT:P29534; GB:M84488; NID:g207642; PIDN:AAA42332.1; PII
A;Cross-references: UNIPROT:P29534; GB:M84488; NID:g207642; PIDN:AAA42332.1; PII
R;Williams, A.; Atkins, R.; Fries, J.; Gimbrone, M.A.; Cybulsky, M.I.; Collins, gubmitted to the EMBL Data Library, February 1992
A;Description: Nucleotide sequence of rat vascular cell adhesion molecule-1.
A;Reference number: S19872
A;Accession: S19872
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A;Accession: JS0675
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                      neural cell adhesion molecule L1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S05479; B60850; S22167
R;Moos, M.; Tacke, R.; Scherer, H.; Teplow, D.; Frueh, K.; Schachner, M.
Nature 334, 701-703, 1988
A;Title: Neural adhesion molecule L1 as a member of the immunoglobulin superfamily with
A;Reference number: S05479; MUID:88318924; PMID:3412448
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A;Cross-references: UNIPROT:D11627; EMBL:X12875; NID:g53336; PIDN:CAA31368.1; A;Note: the authors translated the codon CT for residue 166 as Leu, ACT for r A;Note: part of this sequence, including the amino end of the mature protein, R;Rathjen, F.G.; Wolff, J.M.; Frank, R.; Bonhoeffer, F.; Rutishauser, U. J. Cell Biol. 104, 343-353, 1987
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A; Accession: S05479
                                                                                                                                                                                                       A; Residues: 1-1260 < MOO>
                                                                                                                                                                                                                                    A; Molecule type: mRNA
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Pred. No. 0.028;
0; Mismatches 71
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residue 396
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A;Introns: 26/1; 31/1; 66/2; 133/1; 174/1; 231/1; 268/2; 330/1
A;Introns: 26/1; 31/1; 66/2; 133/1; 174/1; 231/1; 268/2; 330/1
A;Note: the list of introns may be incomplete
A;Note: the list of introns may be incomplete
C;Superfamily: neural cell adhesion molecule L1; fibronectin t
C;Keywords: alternative splicing; cell adhesion; duplication;
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: neural cell adhesion molecule #status exper
F;20-1260/Product: immunoglobulin homology <IMM1>
F;440-498/Domain: immunoglobulin homology <IMM3>
F;531-592/Domain: immunoglobulin homology <IMM3>
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R;Kohl, A.; Giese, K.P.; Mohajeri, M.H.; Montag, D.;
submitted to the EMBL Data Library, December 1991
A;Description: Analysis of promoter activity and 5'
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                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-338 <PIN>
A; Experimental source: brain
C; Comment: This is a neuronal source:
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A; Residues: 1-165, 'L',167-189, 'E',191-281,'S',283-395,'S',397-514,'APEKNPVDV',524,'GEGNET
                                                                                                                                                     C;Genetics:
A;Gene: lamp
C;Superfamily
C;Keywords: b
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R;Pimenta, A.F.; Fische:
Gene 170, 189-195, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 10-May_1996 #sequence_revision 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             limbic-system-associated membrane protein precursor -
                                     F;333-339/Region: hydrophobic F;640,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status F;40,66,136,148,171,220,231/Binding site: phosphate (Thr) (covalent) #status predic F;42,115,142,164,171,220,231/Binding site: phosphate (Ser) (covalent) #status predicted F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S22167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                            Superfamily: carcinoembryonic antigen; carcinoembryonic antigen; keywords: brain; glycoprotein; membrane protein; phosphoprotein; 1.7/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSQLELODSGTWTCTVLQNQKKVEF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DLQERGDSDKYFIEDGK--LVIQSLDYSDQGNYSCVASTELDEVESRAQLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLVF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILANLQVKEATQITQGPRSAIEKKGARVTFTCQASFDPSLQASITWRGDGR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQ--FHWKNSNQIKILGNQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGPVPHLELSDRHLLKQSQVHLSW-----SPAEDHNSPIEKYDIEFEDKEMAPEKWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLTAN----SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fischer, I.; Levitt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - PGNQTSTTLKLSPYVHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124; DB 1
Pred. No. 0.053;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268/2; 330/1; 374/1; 422/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure
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glycoprotein;
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                           "scatus predicted
s predicted
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Query Match Best Local Similarity

11.5%; 23.6%;

Score 118.5; DB Pred. No. 0.031;

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49; Conservative 35; Mismatches 91; Indels 33; Gaps 9  10 LLLVIQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61

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